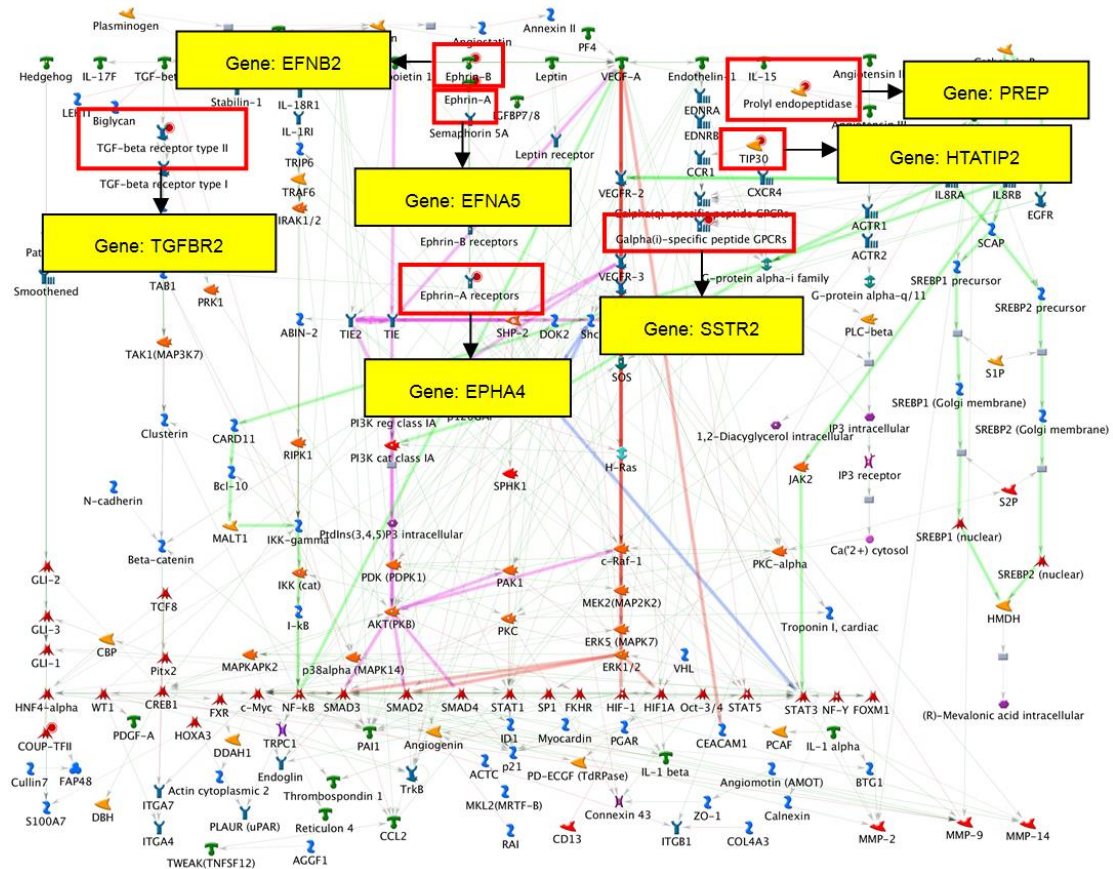


(a)



(b)

Figure S2. Functional annotation for the candidate target genes in *MetaCore* process networks. The red rectangles refer to those genes found in the mapped normal-specific strongly co-expressed gene pairs. (a) “*Cell adhesion\_Attractive and repulsive receptors*” process network. (b) “*Development\_Regulation of angiogenesis*” process network.